Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (Currently Amended) A method of assaying one or more target oligonucleotides in a sample comprising the steps of:

(a) contacting at least one capture oligonucleotide with the sample under suitable hybridization conditions to hybridize any ~~the~~ target oligonucleotide to the capture oligonucleotide, the capture oligonucleotide comprising a molecular recognition sequence comprising at least one non-standard base, the capture oligonucleotide being coupled to a support, the target oligonucleotide comprising a tagging sequence complementary to the molecular recognition sequence of the capture oligonucleotide ~~and an analyte-specific sequence or a complement of the analyte-specific sequence~~; and

(b) detecting hybridization of the target oligonucleotide to the capture oligonucleotide.

2. (Original) The method of claim 1, wherein the support comprises a single solid support.

3. (Original) The method of claim 1, wherein the support comprises a solid particle.

4. (Original) The method of claim 1, wherein the support comprises at least two different types of capture oligonucleotides, the sequences of each type of capture oligonucleotide differing from the molecular recognition sequence of other types of capture oligonucleotides by

at least one base, and wherein the tagging sequence of the target oligonucleotide is complementary to the molecular recognition sequence of one of the types of capture oligonucleotides.

5. (Original) The method of claim 1, wherein at least two different types of capture oligonucleotides are coupled to a plurality of supports, the molecular recognition sequences of each different type of capture oligonucleotide differing by at least one base and wherein each target oligonucleotide comprises a tagging sequence complementary to the molecular recognition sequence of one of the types of capture oligonucleotides.

6. (Currently Amended) The method of claim 5, wherein the plurality of supports form at least two groups, each group having a characteristic that distinguishes its members from members of others groups.

7. (Cancelled)

8. (Original) The method of claim 1, wherein the target oligonucleotide further comprises a reporter or coupling moiety and wherein detecting step comprises detecting the presence of the reporter or coupling moiety associated with the support.

9. (Original) The method of claim 8, wherein the reporter or coupling moiety is associated with a non-standard base.

10. (Cancelled)

11. (Cancelled)

12. (Currently Amended) The method of claim 1, wherein at least one target oligonucleotide is prepared by

contacting an analyte with at least one primer pair, the analyte comprising at least one analyte-specific sequence, each primer pair comprising a first primer and a second primer, the first primer comprising a target oligonucleotide tagging sequence and a sequence complementary to a first sequence of the analyte, the second primer comprising a sequence complementary to a second sequence of the analyte; and

enzymatically extending the first and second primers to form the target oligonucleotide comprising the analyte-specific sequence and a second oligonucleotide sequence complementary to the analyte-specific sequence~~, wherein one of the target oligonucleotide and the second oligonucleotide comprises the analyte-specific sequence and the other comprises a sequence complementary to the analyte-specific sequence~~.

13 (Original). The method of claim 12, wherein the second oligonucleotide comprises a reporter or coupling moiety.

14. (Original) The method of claim 1, wherein the tagging sequence of the target oligonucleotide comprises a first sequence and a second sequence, the first sequence located at the 5' end of the target oligonucleotide and the second sequence located at the 3' end of the target oligonucleotide.

15. (Original) The method of claim 12, wherein the at least one of the first and second primers is a first allele-specific primer, further comprising contacting the analyte with at least one additional allele-specific primer different from the first allele-specific primer.

16. (Original) The method of claim 12, wherein both the target oligonucleotide and the second oligonucleotide comprise a tagging sequence and the capture oligonucleotide

comprises a first molecular recognition sequence and a second molecular recognition sequence coupled to the first molecular recognition sequence through a linker, the first and second molecular recognition sequences being complementary to the tagging sequences of the target oligonucleotide and the second oligonucleotide, respectively.

17. (Original) The method of claim 12, further comprising covalently coupling the second oligonucleotide to the capture oligonucleotide and removing the target oligonucleotide.

18. (Original) The method of claim 17, wherein the step of covalently coupling comprises ligating the second oligonucleotide to the capture oligonucleotide.

19. (Original) A method of assaying a target oligonucleotide in a sample comprising steps of:

(a) contacting a capture oligonucleotide coupled to a support with the sample under suitable hybridization conditions to hybridize a target oligonucleotide, the target oligonucleotide comprising a tagging sequence comprising at least one non-standard base and an analyte-specific sequence or a complement thereof, the capture oligonucleotide comprising a molecular recognition sequence comprising a sequence that is the same as or complementary to the analyte-specific sequence;

(b) enzymatically extending the capture oligonucleotide using the target oligonucleotide as a template and incorporating a complementary non-standard base opposite the non-standard base of the tagging sequence; and

(c) incorporating a reporter or coupling moiety onto an extended portion of the capture oligonucleotide, and

(d) detecting the presence of the target oligonucleotide in the sample by detecting incorporation of the reporter or coupling moiety.

20. (Currently Amended) A method of assaying a target oligonucleotide comprising steps of:

(a) contacting an analyte comprising ~~the~~ an analyte-specific sequence with a first primer and a second primer, the first primer comprising a tagging sequence and a sequence complementary to a first sequence of the analyte, the second primer comprising a sequence complementary to a second sequence of the analyte and a non-standard base;

(b) enzymatically extending the first and second primers to form a target oligonucleotide and a second oligonucleotide, wherein one of the target oligonucleotide and the second oligonucleotide comprises the analyte-specific sequence and the other comprises a sequence complementary to the analyte-specific sequence~~, wherein the extension of the first primer is substantially halted at the position opposite the non-standard base of the second primer~~;

(c) incorporating a complementary non-standard base into the extended first primer opposite the non-standard base of the second primer;

(d) contacting a capture oligonucleotide coupled to a support with the target oligonucleotide under hybridizing conditions to hybridize a target oligonucleotide, the target oligonucleotide comprising the tagging sequence and the analyte-specific sequence or a complement of the analyte-specific sequence, the capture oligonucleotide comprising a molecular

recognition sequence that is ~~the same as or~~ complementary to the tagging sequence of the target oligonucleotide ~~at least a portion of the analyte specific sequence~~; and

(e) detecting hybridization of target oligonucleotide to the capture oligonucleotide.

21. (Currently Amended) A method of ~~simultaneously~~ detecting at least one target oligonucleotide ~~two alleles in a sample comprising genomic DNA~~ comprising the steps of:

(a) contacting the sample with at least one ~~two~~ primer pair ~~pairs~~ comprising a first primer and a second primer under conditions such that the ~~each~~ first and second primer of the primer pair ~~pairs~~ hybridizes to the target oligonucleotide, if present ~~genomic DNA~~;

(b) amplifying the target oligonucleotide, if present ~~DNA sequences flanked by the first and second primer of each primer pair~~;

(c) hybridizing any ~~the~~ amplified target oligonucleotide from ~~DNA sequences of step~~ (b) with at least one ~~two~~ tagged primer ~~, allele specific primers, each tagged, allele specific primer~~ comprising, in 5' to 3' order, a 5' tagging sequence ~~seqeunce~~ comprising at least one non-standard nucleotide~~, a linker~~, and a 3' sequence capable of hybridizing with the ~~an~~ amplified target oligonucleotide from ~~sequence of step~~ (b);

(d) enzymatically extending the at least one ~~allele specific~~ primer of step (c) in the presence of a labeled triphosphate base to form a labeled extension product, the labeled extension product comprising the tagging sequence comprising at least one non-standard base ~~products~~;

(e) contacting the labeled extension product ~~products~~ of step (d) with at least one ~~two~~ capture oligonucleotide comprising a molecular recognition sequence complementary to the

tagging sequence of the labeled extension product and ~~oligonucleotides~~ coupled to a support under suitable hybridization conditions to hybridize the labeled ~~an~~ extension product~~, the extension product comprising a tagging sequence comprising at least one non-standard base and an allele-specific sequence, the capture oligonucleotide comprising a molecular recognition sequence comprising a sequence complementary to the tagging sequence, the molecular recognition sequence comprising a non-standard base complementary to the non-standard base of the~~; and

(f) detecting the hybridization of (e) ~~at least to extension product to at least two capture oligonucleotides~~.

22. (Currently Amended) The method of claim 21, wherein at least one primer of each primer pair of step (a) comprises at least one ~~a first~~ non-standard base, wherein the extension product of the primer is complementary to the ~~allele-specific~~ primer of step (c), wherein a labeled non-standard triphosphate base of step (d) is complementary to the first non-standard base of the primer of step (a), and wherein the extension product of step (d) comprises a labeled second non-standard base opposite the first non-standard base of the extension product of the primer comprising the first non-standard base.

23. (Cancelled)

24. (Currently Amended) A method of assaying at least two target oligonucleotides comprising the steps of:

(a) contacting an analyte comprising an ~~the~~ analyte-specific sequence with a first primer and a second primer, the second primer comprising, in 5' to 3' order, a ~~non-~~

~~complementary~~ sequence that is not complementary to the analyte-specific sequence, a non-standard base, and an analyte-specific sequence;

(b) enzymatically extending the primers of (a) to form an extension product ~~to form a target oligonucleotide and a second oligonucleotide, wherein one of the target oligonucleotide and the second oligonucleotide comprises the analyte-specific sequence and the other comprises a sequence complementary to the analyte-specific sequence~~;

(c) hybridizing to the extension product of the second primer of step (b) at least one tagged~~, allele-specific~~ primer comprising, in 5' to 3' order, a 5' tagging sequence comprising at least one non-standard base~~, a linker,~~ and a 3' sequence complementary to the extension product of the second primer;

(d) enzymatically extending the tagged ~~allele-specific~~ primer of step (c);

(e) hybridizing a reporter oligonucleotide complementary to the ~~5' non-complementary~~ sequence that is not complementary to the analyte-specific sequence of the second primer of step (a) to the extension product of step (b) ~~(d), the reporter oligonucleotide comprising a 5' phosphate and a reporter moiety, to form a nick structure suitable for ligation by a ligase;~~

(f) contacting the tagged extension product of step (d) with at least one capture oligonucleotide comprising at least one non-standard nucleotide and coupled to a support under suitable hybridization conditions to hybridize the tagged extension product to the at least one capture oligonucleotide ~~nick structure of step (e) with a ligase to ligate the reporter oligonucleotide to the allele-specific extension product;~~

~~(g) contacting a capture oligonucleotide coupled to a support with the ligation product of step (f)~~; and

(g) ~~(h)~~ detecting the hybridization of (f). ~~ligated oligonucleotide to the capture oligonucleotide~~

25. (Original) A kit for assaying an analyte, the kit comprising:

a support,

capture oligonucleotides coupled to the support, the capture oligonucleotides comprising a molecular recognition sequence having at least one non-standard base;

first primers comprising a tagging sequence and a sequence complementary to a first sequence of the analyte; and

second primers comprising a sequence complementary to a second sequence of the analyte.

26. (Currently Amended) A method of assaying a target oligonucleotide comprising steps of:

(a) contacting an analyte comprising ~~the~~ an analyte-specific sequence with a first primer and a second primer, the second primer comprising, in 5' to 3' order, a ~~non-complementary~~ sequence that is not complementary to the analyte-specific sequence, a non-standard base, and an analyte-specific sequence;

(b) enzymatically extending the primers to form a target oligonucleotide and a second oligonucleotide, wherein one of the target oligonucleotide and the second oligonucleotide

comprises the analyte-specific sequence and the other comprises a sequence complementary to the analyte-specific sequence;

(c) hybridizing to the extension product of the second primer of step (b) a tagged, allele-specific primer comprising, in 5' to 3' order, a 5' tagging sequence comprising a non-standard base, a linker, and a 3' sequence complementary to the extension product of the second primer;

(d) enzymatically extending the allele-specific primer of step (c);

(e) hybridizing a reporter oligonucleotide complementary to the ~~5' non-complementary~~ sequence that is not complementary to the analyte-specific sequence of the second primer of step (a) to the extension product of step (d);

(f) contacting a capture oligonucleotide coupled to a support with the product of step (f); and

(g) detecting hybridization of the reporter oligonucleotide to the capture oligonucleotide.

27. (New) The method of claim 1 wherein (a) is conducted at room temperature.

28. (New) The method of claim 1 wherein (a) is not followed by a washing.

29. (New) The method of claim 20 wherein (d) is conducted at room temperature.

30. (New) The method of claim 20 wherein (d) is not followed by a washing.

31. (New) The method of claim 21 wherein (e) is conducted at room temperature.

32. (New) The method of claim 21 wherein (e) is not followed by a washing.

33. (New) The method of claim 24 wherein (f) is conducted at room temperature.

34. (New) The method of claim 24 wherein (f) is not followed by a washing.

35. (New) The method of claim 24 further comprising covalently attaching the extension product of (d) to the reporter oligonucleotide of (e) with a ligase.

36. (New) The method of claim 17 wherein removing the target oligonucleotide comprises washing.

37. (New) A method of assaying at least two target oligonucleotides in a sample comprising the steps of:

(a) contacting at least two capture oligonucleotides with the sample under suitable hybridization conditions to hybridize the at least two different target oligonucleotides to the at least two capture oligonucleotides, the at least two different capture oligonucleotides each comprising a molecular recognition sequence comprising at least one non-standard base, the at least two different capture oligonucleotides being coupled to a support, the at least two different target oligonucleotides each comprising a tagging sequence complementary to the molecular recognition sequence of the at least two different capture oligonucleotides and an analyte-specific sequence or a complement of the analyte-specific sequence; and

(b) detecting the hybridization of the at least two different target oligonucleotides to the at least two different capture oligonucleotides.

38. (New) The method of claim 37 wherein (a) is conducted at room temperature.

39. (New) The method of claim 37 wherein (a) is not followed by a washing.